



## SEQUENCE LISTING

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<120> H. Pylori Fucosyltransferases

<130> 019957-019400US

<140> US 10/764,212

<141> 2004-01-22

<160> 81

<170> PatentIn Ver. 2.1

<210> 1

<211> 1461

<212> DNA

<213> Helicobacter pylori

<220>

<223> H. pylori strain 1182 FutB fucosyltransferase  
(1182B)

<400> 1

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<212> PRT

<213> Helicobacter pylori

<220>

<223> H. pylori strain 1182 FutB fucosyltransferase

<400> 2

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Trp	Trp	Gly	Asp	Glu	Glu	Val	Glu	Glu	Phe	Lys	Lys	Asn	Ile	Leu	Tyr	
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Glu	Pro	Ser	Asp	Leu	Val	Phe	Gly	Ser	Pro	Ile	Gly	Ser	Ala	Arg	Lys	
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Leu Asp Met Leu Tyr Glu Asn Pro Leu Asn Thr Leu Asp Gly Lys Ala  
 305 310 315 320  
 Tyr Phe Tyr Gln Asn Leu Ser Phe Lys Lys Ile Leu Asp Phe Phe Lys  
 325 330 335  
 Thr Ile Leu Glu Asn Asp Thr Ile Tyr His Asp Asn Pro Phe Ile Phe  
 340 345 350  
 Tyr Arg Asp Leu Asn Glu Pro Leu Ile Ser Ile Asp Asp Asp Leu Arg  
 355 360 365  
 Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn  
 370 375 380  
 Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp  
 385 390 395 400  
 Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu  
 405 410 415  
 Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val  
 420 425 430  
 Asn Tyr Asp Asp Leu Arg Val Asn Tyr Glu Arg Leu Leu Gln Asn Ala  
 435 440 445  
 Ser Pro Leu Leu Glu Leu Ser Gln Asn Thr Thr Phe Lys Ile Tyr Arg  
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<210> 3

<211> 1299

<212> DNA

<213> *Helicobacter pylori*

<220>

<223> *H. pylori* strain 1111 FutA fucosyltransferase  
(1111FutA)

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 tttaaaaaga gcgttcttta ttttattccta agccagcatt acacaatcac tttacaccga 180  
 aaccctgata aacctgcgga catcgtcttt ggtaaccccc ttggatcagc cagaaaaatc 240  
 ttatcctatc aaaacgcaaa aagggtgttt tacaccggtg aaaatgaagt ccctaacttc 300  
 aacctctttg attacgccat aggctttgat gaattggact ttagagatcg ttatttgaga 360  
 atgcctttgt attatgccta tttgcattat aaagccgagc ttgttaatga caccacttcg 420  
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 tttgcgagct ttgtcgcaag caaccctaac gctcctagaa ggaacgcttt ttatgaggct 600  
 ttaaacgcta ttgagccagt tgctggggga gggagcgtga aaaacacttt aggctataat 660  
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ttttacaaa atttgagttt taaaaaaatc ctagattttt ttaaaacgat tttagaaaac 1020
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<210> 4

<211> 432

<212> PRT

<213> Helicobacter pylori

<220>

<223> H. pylori strain 1111 FutA fucosyltransferase

<400> 4

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             20             25             30

Trp Gly Asp Glu Glu Ile Lys Lys Phe Lys Lys Ser Val Leu Tyr Phe
             35             40             45

Ile Leu Ser Gln His Tyr Thr Ile Thr Leu His Arg Asn Pro Asp Lys
             50             55             60

Pro Ala Asp Ile Val Phe Gly Asn Pro Leu Gly Ser Ala Arg Lys Ile
             65             70             75             80

Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn Glu
             85             90             95

Val Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu Leu
             100            105            110

Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Ala Tyr Leu
             115            120            125

His Tyr Lys Ala Glu Leu Val Asn Asp Thr Thr Ser Pro Tyr Lys Leu
             130            135            140

Gln Pro Asp Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His Phe Lys
             145            150            155            160

Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asn Glu Ser Asp Pro
             165            170            175

Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Pro Asn Ala Pro
             180            185            190

Arg Arg Asn Ala Phe Tyr Glu Ala Leu Asn Ala Ile Glu Pro Val Ala
             195            200            205

Gly Gly Gly Ser Val Lys Asn Thr Leu Gly Tyr Asn Val Lys Asn Lys
             210            215            220

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 Asp Met His Tyr Glu Asn Pro Leu Asn Thr Ile Asp Gly Lys Ala Tyr  
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 Phe Tyr Gln Asn Leu Ser Phe Lys Lys Ile Leu Asp Phe Phe Lys Thr  
 325 330 335  
 Ile Leu Glu Asn Asp Thr Ile Tyr His Asp Asn Pro Phe Ile Phe Tyr  
 340 345 350  
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 355 360 365  
 Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp  
 370 375 380  
 Asp Leu Arg Val Asn Tyr Glu Arg Leu Leu Gln Asn Ala Ser Pro Leu  
 385 390 395 400  
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<210> 5  
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 <223> *H. pylori* strain 1218 FutB fucosyltransferase  
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 gaatttaaaa agaacattct ttattttatt ctgagtcagc attacacaat caccctccac 180  
 caaaacccca acgaaccctc cgatctcgtc tttggcagtc ctattggatc agccagaaaa 240  
 atcttatcct atcaaaacgc aaaaagagtg ttttacaccg gtgaaaacga atcgccctaat 300  
 ttcaacctct ttgattacgc cataggcttt gatgaattgg atttttagaga tcgttattta 360  
 agaatgcctt tatattatga tagactacac cataaagccg agagcgtgaa tgacaccact 420  
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cctattttatt gggggagtc tagcgtggca caagatttta accctaagag ttttgtgaat 840
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<210> 6

<211> 485-

<212> PRT

<213> Helicobacter pylori

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<223> H. pylori strain 1218 FutB fucosyltransferase

<400> 6

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Trp Trp Gly Asp Glu Glu Val Glu Glu Phe Lys Lys Asn Ile Leu Tyr
      35                      40                      45

Phe Ile Leu Ser Gln His Tyr Thr Ile Thr Leu His Gln Asn Pro Asn
      50                      55                      60

Glu Pro Ser Asp Leu Val Phe Gly Ser Pro Ile Gly Ser Ala Arg Lys
      65                      70                      75                      80

Ile Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn
          85                      90                      95

Glu Ser Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu
      100                      105                      110

Leu Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Asp Arg
      115                      120                      125

Leu His His Lys Ala Glu Ser Val Asn Asp Thr Thr Ser Pro Tyr Lys
      130                      135                      140

Leu Lys Pro Asp Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His Phe
      145                      150                      155                      160

Lys Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asn Glu Ser Asp
          165                      170                      175

Pro Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Pro Asn Ala
      180                      185                      190

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 210 215 220  
 Lys Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu Asn  
 225 230 235 240  
 Ser Gln Gly Tyr Gly Tyr Val Thr Glu Lys Ile Ile Asp Ala Tyr Phe  
 245 250 255  
 Ser His Thr Ile Pro Ile Tyr Trp Gly Ser Pro Ser Val Ala Gln Asp  
 260 265 270  
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 275 280 285  
 Glu Ala Ile Asp His Val Arg Tyr Leu His Thr His Pro Asn Ala Tyr  
 290 295 300  
 Leu Asp Met Leu Tyr Glu Asn Pro Leu Asn Thr Leu Asp Gly Lys Ala  
 305 310 315 320  
 Tyr Phe Tyr Gln Asn Leu Ser Phe Lys Lys Ile Leu Asp Phe Phe Lys  
 325 330 335  
 Thr Ile Leu Glu Asn Asp Thr Ile Tyr His Asp Asn Pro Phe Ile Phe  
 340 345 350  
 Tyr Arg Asp Leu Asn Glu Pro Leu Ile Ser Ile Asp Asp Leu Arg Val  
 355 360 365  
 Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr  
 370 375 380  
 Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp  
 385 390 395 400  
 Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg  
 405 410 415  
 Val Asn Tyr Asp Asp Leu Arg Val Asn Cys Asp Asp Leu Arg Val Asn  
 420 425 430  
 Tyr Asp Asp Leu Arg Val Asn Tyr Glu Arg Leu Leu Gln Asn Ala Ser  
 435 440 445  
 Pro Leu Leu Glu Leu Ser Gln Asn Thr Thr Phe Lys Ile Tyr Arg Lys  
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 Ala Tyr Gln Lys Ser Leu Pro Leu Leu Arg Ala Ala Arg Lys Leu Ile  
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<210> 7  
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 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 ggggtttagaa aaaaatttat cttacatttc attttaagtc agcattacac aatcgctctc 180  
 caccgaaacc ctgataaacc tgcggacatc gtttttggtt acccccttgg atcagccaga 240  
 aaaatcctat cctatcaaaa cgctaaaagg gtgtttttaca ccggtgaaaa cgaagtcctc 300  
 aatttcaacc tctttgatta cgccataggc tttgatgaat tggacttttag agatcgttat 360  
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 <213> Helicobacter pylori

<220>  
 <223> H. pylori strain 19C2 FutB fucosyltransferase

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 Pro Leu Asp Lys Arg Glu Ser Lys Gly Phe Arg Lys Lys Phe Ile Leu  
 35 40 45  
 His Phe Ile Leu Ser Gln His Tyr Thr Ile Ala Leu His Arg Asn Pro  
 50 55 60  
 Asp Lys Pro Ala Asp Ile Val Phe Gly Asn Pro Leu Gly Ser Ala Arg  
 65 70 75 80  
 Lys Ile Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu  
 85 90 95  
 Asn Glu Val Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp  
 100 105 110  
 Glu Leu Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Asp  
 115 120 125  
 Arg Leu His His Lys Ala Glu Ser Val Asn Asp Thr Thr Ala Pro Tyr  
 130 135 140



Lys Ile Lys Ser Asp Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His  
 145 150 155 160  
 Phe Lys Glu Asn His Pro His Leu Cys Ala Leu Ile Asn Asn Glu Ile  
 165 170 175  
 Asp Pro Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Pro Asn  
 180 185 190  
 Ala Pro Ile Arg Asn Ala Phe Tyr Glu Ala Leu Asn Ser Ile Glu Pro  
 195 200 205  
 Val Thr Gly Gly Gly Ser Val Arg Asn Thr Leu Gly Tyr Asn Val Lys  
 210 215 220  
 Asn Lys Asn Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu  
 225 230 235 240  
 Asn Thr Gln Gly Tyr Gly Tyr Val Thr Glu Lys Ile Ile Asp Ala Tyr  
 245 250 255  
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<210> 9  
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 <212> DNA  
 <213> Helicobacter pylori

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 ttacaccgaa accctgataa acctgcggac atcgtctttg gtaacccct tggatcagcc 180  
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 <212> PRT  
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<220>  
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 (915A.pcpneose)

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 Ala Asp Ile Val Phe Gly Asn Pro Leu Gly Ser Ala Arg Lys Ile Leu  
           50                                  55                                  60  
 Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn Glu Val  
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 Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe  
                                   85                                  90

<210> 11  
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 <212> DNA  
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           (26695A.cod)

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 aaagaattta aaaagagcgt tctttatatt atcctaagcc aacgctacgc aatcaccctc 180  
 caccaaaacc ccaatgaatt ttcagatcta gtttttagca atcctcttgg agcggctaga 240  
 aagattttat cttatcaaaa cactaaacga gtgttttaca ccggtgaaaa cgaatcacct 300  
 aatttcaacc tctttgatta cgccataggc tttgatgaat tggattttta tgatcgttat 360  
 ttgagaatgc ctttgtatta tgcccatttg cactataaag ccgagcttgt taatgacacc 420  
 actgcgcctt acaaactcaa agacaacagc ctttatgctt taaaaaaacc ctctcatcat 480  
 tttaaagaaa accaccctaa tttgtgcgca gtagtgaatg atgagagcga tcttttaaaa 540  
 agagggtttg ccagttttgt agcgagcaac gctaacgctc ctatgaggaa cgctttttat 600  
 gacgctctaa attccataga gccagttact gggggaggaa gtgtgagaaa cacttttaggc 660  
 tataaggttg gaaacaaaag cgagttttta agccaatata agttcaatct ctgttttgaa 720  
 aactcgcaag gttatggcta tgtaaccgaa aaaatccttg atgcgtattt tagccatacc 780  
 attcctattt attgggggag tcccagcgtg gcgaaagatt ttaaccctaa aagttttgtg 840  
 aatgtgcatg atttcaacaa ctttgatgaa gcgattgatt atatcaaata cctgcacacg 900  
 cacccaaacg cttattttaga catgctctat gaaaaccctt taaacaccct tgatgggaaa 960  
 gttacttttt accaagattt gagtttttaa aaaatcctag atttttttaa aacgatttta 1020  
 gaaaacgata cgattttatca caaatttctca acatctttca tgtgggagta cgatctgcat 1080  
 aagccggttag tatccattga tgatttgagg gttaattatg atgatttgag gggttaattat 1140  
 gaccggcttt tacaaaacgc ttcgccttta ttagaactct ctcaaaacac cactttttaa 1200  
 atctatcgca aagcttatca aaaatccttg ctttgttggc gcgcggtgag aaagtgggtt 1260  
 aaaaaattgg gtttgtaa 1278

<210> 12  
 <211> 425  
 <212> PRT  
 <213> Helicobacter pylori

<220>  
 <223> H. pylori strain 26695 FutA fucosyltransferase

<400> 12  
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       1                                  5                                  10                                  15  
 Lys Met Ala Ser Lys Ser Pro Pro Pro Pro Leu Lys Ile Ala Val Ala  
           20                                  25                                  30

Asn Trp Trp Gly Asp Glu Glu Ile Lys Glu Phe Lys Lys Ser Val Leu  
 35 40 45  
 Tyr Phe Ile Leu Ser Gln Arg Tyr Ala Ile Thr Leu His Gln Asn Pro  
 50 55 60  
 Asn Glu Phe Ser Asp Leu Val Phe Ser Asn Pro Leu Gly Ala Ala Arg  
 65 70 75 80  
 Lys Ile Leu Ser Tyr Gln Asn Thr Lys Arg Val Phe Tyr Thr Gly Glu  
 85 90 95  
 Asn Glu Ser Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp  
 100 105 110  
 Glu Leu Asp Phe Asn Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Ala  
 115 120 125  
 His Leu His Tyr Lys Ala Glu Leu Val Asn Asp Thr Thr Ala Pro Tyr  
 130 135 140  
 Lys Leu Lys Asp Asn Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His  
 145 150 155 160  
 Phe Lys Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asp Glu Ser  
 165 170 175  
 Asp Leu Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Ala Asn  
 180 185 190  
 Ala Pro Met Arg Asn Ala Phe Tyr Asp Ala Leu Asn Ser Ile Glu Pro  
 195 200 205  
 Val Thr Gly Gly Gly Ser Val Arg Asn Thr Leu Gly Tyr Lys Val Gly  
 210 215 220  
 Asn Lys Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu  
 225 230 235 240  
 Asn Ser Gln Gly Tyr Gly Tyr Val Thr Glu Lys Ile Leu Asp Ala Tyr  
 245 250 255  
 Phe Ser His Thr Ile Pro Ile Tyr Trp Gly Ser Pro Ser Val Ala Lys  
 260 265 270  
 Asp Phe Asn Pro Lys Ser Phe Val Asn Val His Asp Phe Asn Asn Phe  
 275 280 285  
 Asp Glu Ala Ile Asp Tyr Ile Lys Tyr Leu His Thr His Pro Asn Ala  
 290 295 300  
 Tyr Leu Asp Met Leu Tyr Glu Asn Pro Leu Asn Thr Leu Asp Gly Lys  
 305 310 315 320  
 Ala Tyr Phe Tyr Gln Asp Leu Ser Phe Lys Lys Ile Leu Asp Phe Phe  
 325 330 335  
 Lys Thr Ile Leu Glu Asn Asp Thr Ile Tyr His Lys Phe Ser Thr Ser  
 340 345 350

Phe Met Trp Glu Tyr Asp Leu His Lys Pro Leu Val Ser Ile Asp Asp  
           355                                  360                                  365  
 Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Arg Leu Leu  
           370                                  375                                  380  
 Gln Asn Ala Ser Pro Leu Leu Glu Leu Ser Gln Asn Thr Thr Phe Lys  
           385                                  390                                  395                                  400  
 Ile Tyr Arg Lys Ala Tyr Gln Lys Ser Leu Pro Leu Leu Arg Ala Val  
                                   405                                  410                                  415  
 Arg Lys Leu Val Lys Lys Leu Gly Leu  
                                   420                                  425

<210> 13  
 <211> 45 -  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <223> H. pylori strain 19C2 fucosyltransferase  
           (19C2FutA.cod)

<400> 13  
 atgttccaac ccttactaga cgcctttata gaaagtgctc caatt

45

<210> 14  
 <211> 15  
 <212> PRT  
 <213> Helicobacter pylori

<220>  
 <223> H. pylori strain 19C2 fucosyltransferase  
           (19C2A.pep)

<400> 14  
 Met Phe Gln Pro Leu Leu Asp Ala Phe Ile Glu Ser Ala Pro Ile  
       1                                  5                                  10                                  15

<210> 15  
 <211> 1973  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <223> H. pylori strain 1111 FutB fucosyltransferase

<400> 15  
 ggatcccagag cgaccaatca ttacagggat ttattgcatt tagatgcggc tttcagtaac 60  
 acgctgatcg tggaaaataa cgccttaaac ggcttggtta cggggcatat gatgttttca 120  
 cattctaaag gcgaaatgct cctcgctttg caacgctcgt tgaatatcag taaagatcgc 180  
 acttttagtcg tgggcgatgg ggcgaatgat ttgagcatgt tcaaacatgc ccatattaaa 240  
 atcgctttta acgctaaaga ggttttataa cagcacgcca cgcattgcat caatgagcct 300  
 aatctagccc taatcaagcc tttgatttac aaaaattttt tttgtaaaat tccctttaaa 360  
 aggatagcca tgttccaacc cctattagac gcttatgtag aaagcgcttc cattgaaaaa 420  
 atggcctcta aatctcccc cccctataaa atcgctgtgg cgaattggtg gggagatgaa 480  
 gaaattaaag aatttaaaaa gagcgttctt tattttatct ttagccaacg ctacacaatc 540

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gccctccacc aaaaccccaa tgaattttca gatctagtct ttagcaatcc tcttggatca 600
gctagaaaaa tcttatcgta tcaaaacgct aaaagagtgt tttacaccgg tgaaaatgaa 660
gtccctaact tcaacctctt tgattacgcc ataggctttg atgaattgga ttttagagat 720
cgttatttga ggatgccttt atattatgat aggctacacc ataaagccga gagcgtgaat 780
gacaccactt cgccctacaa actcaaagac aacagccttt atactttaaa aaaaccctcc 840
catcaattta aagaaaacca ccctaattta gcgcagtcgt gaatgatgag agcgatcctt 900
tgaaaagagg ggttgtgagc tttgtagcga gcaacgctaa cgctcctatg agaaacgcct 960
tttatgacgc tttaaattct attgagccag ttactggggg agggagcgtg aaaaacactt 1020
taggctataa cgtcaaaaac aagagcgagt ttttaagcca atacaagttc aacctgtgtt 1080
ttgaaaactc acaaggctat ggctatgtaa ccgagaagat ccttgacgct tacttttagcc 1140
acaccattcc tatttatttg gggagtccta gcgtggcgaa agattttaac cctaaagagt 1200
ttgtgaatgt ccatgatttc aacaactttg atgaagcgat agattataac aaatacttgc 1260
acacgcaccc aaacgcttat ttagacatgc tctatgaaaa ccctttaaac gcccttgatg 1320
ggaaagctta cttttaccag gatttgagtt ttaaaaaaat cctagctttt tttaaaacga 1380
ttttagaaaa cgatacgatt tatcacaaat cctcaacatc tttcatgtgg agtgcgatct 1440
cgatgagccg ttagcgtcta ttgatgattt gaggggttaat tatgatgatt tgaggggttaa 1500
ttatgatgat ttgaggggtta attatgatga tttgaggggt aattatgatg atttgagggg 1560
taattatgat gatttgaggg ttaattatag cgccttttgc aaaacgcttc acctttattg 1620
gaattatccc aaaacacctc ttttaaaatc tatcgcaaag cctatcaaag cctatcaaaa 1680
atccttacc cttattgcgc ccataaggag atgggttaaa aagtaagggt tcttttaaga 1740
ctgggtgaga aattgaagcg ctattttaaa atgcgctaac gcttctttt tgagcgtggg 1800
gtttttgagc atgtcctcta aagcatgggc gcttaaaaaa tgtttgatt ttaaagacac 1860
gatgcgcca aagattctt ctttagaaa gtttaaaagg cgtttgggca aaatctcgcc 1920
aaatacgata atgacttttg aagcgtgtt gtctaattgc caggtcggaa ttc 1973

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<210> 16

<211> 446

<212> PRT

<213> *Helicobacter pylori*

<220>

<223> *H. pylori* strain 1111 FutB fucosyltransferase

<400> 16

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Met Phe Gln Pro Leu Leu Asp Ala Tyr Val Glu Ser Ala Ser Ile Glu
  1              5              10              15

```

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Lys Met Ala Ser Lys Ser Pro Pro Pro Leu Lys Ile Ala Val Ala Asn
      20              25              30

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```

Trp Trp Gly Asp Glu Glu Ile Lys Glu Phe Lys Lys Ser Val Leu Tyr
    35              40              45

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```

Phe Ile Phe Ser Gln Arg Tyr Thr Ile Ala Leu His Gln Asn Pro Asn
    50              55              60

```

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Glu Phe Ser Asp Leu Val Phe Ser Asn Pro Leu Gly Ser Ala Arg Lys
    65              70              75              80

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```

Ile Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn
      85              90              95

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```

Glu Val Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu
    100              105              110

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Leu Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Asp Arg
    115              120              125

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Leu His His Lys Ala Glu Ser Val Asn Asp Thr Thr Ser Pro Tyr Lys
    130              135              140

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Leu Lys Asp Asn Ser Leu Tyr Thr Leu Lys Lys Pro Ser His Gln Phe  
 145 150 155 160  
 Lys Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asp Glu Ser Asp  
 165 170 175  
 Pro Leu Lys Arg Gly Val Val Ser Phe Val Ala Ser Asn Ala Asn Ala  
 180 185 190  
 Pro Met Arg Asn Ala Phe Tyr Asp Ala Leu Asn Ser Ile Glu Pro Val  
 195 200 205  
 Thr Gly Gly Gly Ser Val Lys Asn Thr Leu Gly Tyr Asn Val Lys Asn  
 210 215 220  
 Lys Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu Asn  
 225 230 235 240  
 Ser Gln Gly Tyr Gly Tyr Val Thr Glu Lys Ile Leu Asp Ala Tyr Phe  
 245 250 255  
 Ser His Thr Ile Pro Ile Tyr Trp Gly Ser Pro Ser Val Ala Lys Asp  
 260 265 270  
 Phe Asn Pro Lys Glu Phe Val Asn Val His Asp Phe Asn Asn Phe Asp  
 275 280 285  
 Glu Ala Ile Asp Tyr Ile Lys Tyr Leu His Thr His Pro Asn Ala Tyr  
 290 295 300  
 Leu Asp Met Leu Tyr Glu Asn Pro Leu Asn Ala Leu Asp Gly Lys Ala  
 305 310 315 320  
 Tyr Phe Tyr Gln Asp Leu Ser Phe Lys Lys Ile Leu Ala Phe Phe Lys  
 325 330 335  
 Thr Ile Leu Glu Asn Asp Thr Ile Tyr His Lys Ser Ser Thr Ser Phe  
 340 345 350  
 Met Trp Glu Cys Asp Leu Asp Glu Pro Leu Ala Ser Ile Asp Asp Leu  
 355 360 365  
 Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val  
 370 375 380  
 Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr  
 385 390 395 400  
 Asp Asp Leu Arg Val Asn Tyr Glu Arg Leu Leu Gln Asn Ala Ser Pro  
 405 410 415  
 Leu Leu Glu Leu Ser Gln Asn Thr Ser Phe Lys Ile Tyr Arg Lys Ala  
 420 425 430  
 Tyr Gln Lys Pro Ile Lys Asn Pro Tyr Pro Tyr Cys Ala Pro  
 435 440 445

<210> 17  
 <211> 1861  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <223> H. pylori strain 802 FutA fucosyltransferase

<400> 17  
 ggatcccggc gtgaattact acctttcttg cttgcacagc tatgccgcag gcgatccctt 60  
 gcctatccct actttcttat actttttggt agcgatacct tttgctctcg tgattttggc 120  
 ttattttcaaa cgccatttga gtttgccctaa attggtttta aggatagcca tgttccagcc 180  
 cttactagac gccttttatag aaagtgcctc aattaaaaaa atgcctctga gttacccccc 240  
 cctaaaaatc gctgtggcga attggtgggg aggcgctgaa gaatttataa agagcgctat 300  
 gtatttcctc ctaagccaac gctacacaat caccctccac caaaacccca acgaaccctc 360  
 cgatctcgtc tttggcagtc ctattggagc agccagaaaa atcctatcct accaaaacac 420  
 taaaagagtg ttttacgccg gtgaaaatga agtcctaat ttcaacctct ttgattacgc 480  
 cataggcttt-gatgaattgg atttttagaga tcggtatttg agaatgcctt tatattatga 540  
 tagactacac cataaagccg agagcgtgaa tgacaccacc gcgccttaca agattaaacc 600  
 tgacagcctt tatacttttaa aaaaaccctc ccatacattt aaagaaaaaac acccccattt 660  
 atgcgcagta gtgaatgatg agagcgatcc tttgaaaaga gggtttgcca gttttgtcgc 720  
 aagcaaccct aacgctccta aaaggaacgc cttctatgac gctttaaatt ctattgagcc 780  
 agttactggg ggagggagcg tgaaaaacac tttaggctat aaagttggaa acaaaaacga 840  
 gtttttaagc caatacaaat tcaatctgtg ttttgaaaac tctcaaggct atggctatgt 900  
 aaccgaaaaa atcattgacg cttacttttag ccataccatt cctattttatt gggggagtcc 960  
 tagcgtggcg aaagatttta accctaagag ttttgtgaat gtgcatgatt ttaaaaactt 1020  
 tgatgaagcg attgattacg tgagatactt gcacacgcac ccaaacgctt atttagacat 1080  
 gctctatgaa aacccttttaa acacccttga tgggaaagct tactttttacc aagatttgag 1140  
 ttttaaaaaa atcctagatt tttttaaaac gatttttagaa aacgatacga tctatcacia 1200  
 taaccctttt gttttctatc gtgatttgaa tgagccgtta gtatctattg atgatttgag 1260  
 agccgattat aataatttga gagccgatta taataatttg agagccgatt ataataattt 1320  
 gagagccgat tataataatt tgagagccga ttacgatcgc ctgttacaaa accgttcgcc 1380  
 tttgttgga ctctctcaaa acaccacttt taaaatctat cacaaaagctt atcacaaatc 1440  
 cttacctttg ttgcgtgcca taaggagatg gggttaaaaaa ttgggtttgt aaaattgggg 1500  
 gtaatcaaac cccttgcgct atcatcgag acgccacttt tctaaaacca gcgatattag 1560  
 cccctaaaac aaaattagta gggctcttaa actcttttagc ggtttgagag acatttttat 1620  
 aaatctcttt catgatgtgg tgtaatttcg catccaccac ttcaaaaactc caaggggtgca 1680  
 tgctcgcggt ttgcgccatt tccaagccgc tcacgctcac cccccagca ttagccgcct 1740  
 tgccataacc ataagaaatc ttagcctgta aaaacaattc aatcgcttca ttgcttgagg 1800  
 gcatgttcgc cccttcagcc acgcatttgc acccattaga aaggagggtt ttgcggaatt 1860  
 c 1861

<210> 18  
 <211> 440  
 <212> PRT  
 <213> Helicobacter pylori

<220>  
 <223> H. pylori strain 802 FutA fucosyltransferase

<400> 18  
 Met Phe Gln Pro Leu Leu Asp Ala Phe Ile Glu Ser Ala Ser Ile Lys  
 1 5 10 15  
 Lys Met Pro Leu Ser Tyr Pro Pro Leu Lys Ile Ala Val Ala Asn Trp  
 20 25 30  
 Trp Gly Gly Ala Glu Glu Phe Lys Lys Ser Ala Met Tyr Phe Ile Leu  
 35 40 45

Ser Gln Arg Tyr Thr Ile Thr Leu His Gln Asn Pro Asn Glu Pro Ser  
 50 55 60  
 Asp Leu Val Phe Gly Ser Pro Ile Gly Ala Ala Arg Lys Ile Leu Ser  
 65 70 75 80  
 Tyr Gln Asn Thr Lys Arg Val Phe Tyr Ala Gly Glu Asn Glu Val Pro  
 85 90 95  
 Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu Leu Asp Leu  
 100 105 110  
 Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Asp Arg Leu His His  
 115 120 125  
 Lys Ala Glu Ser Val Asn Asp Thr Thr Ala Pro Tyr Lys Ile Lys Pro  
 130 135 140  
 Asp Ser Leu Tyr Thr Leu Lys Lys Pro Ser His His Phe Lys Glu Lys  
 145 150 155 160  
 His Pro His Leu Cys Ala Val Val Asn Asp Glu Ser Asp Pro Leu Lys  
 165 170 175  
 Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Pro Asn Ala Pro Lys Arg  
 180 185 190  
 Asn Ala Phe Tyr Asp Ala Leu Asn Ser Ile Glu Pro Val Thr Gly Gly  
 195 200 205  
 Gly Ser Val Lys Asn Thr Leu Gly Tyr Lys Val Gly Asn Lys Asn Glu  
 210 215 220  
 Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu Asn Ser Gln Gly  
 225 230 235 240  
 Tyr Gly Tyr Val Thr Glu Lys Ile Ile Asp Ala Tyr Phe Ser His Thr  
 245 250 255  
 Ile Pro Ile Tyr Trp Gly Ser Pro Ser Val Ala Lys Asp Phe Asn Pro  
 260 265 270  
 Lys Ser Phe Val Asn Val His Asp Phe Lys Asn Phe Asp Glu Ala Ile  
 275 280 285  
 Asp Tyr Val Arg Tyr Leu His Thr His Pro Asn Ala Tyr Leu Asp Met  
 290 295 300  
 Leu Tyr Glu Asn Pro Leu Asn Thr Leu Asp Gly Lys Ala Tyr Phe Tyr  
 305 310 315 320  
 Gln Asp Leu Ser Phe Lys Lys Ile Leu Asp Phe Phe Lys Thr Ile Leu  
 325 330 335  
 Glu Asn Asp Thr Ile Tyr His Asn Asn Pro Phe Val Phe Tyr Arg Asp  
 340 345 350  
 Leu Asn Glu Pro Leu Val Ser Ile Asp Asp Leu Arg Ala Asp Tyr Asn  
 355 360 365



Asn Leu Arg Ala Asp Tyr Asn Asn Leu Arg Ala Asp Tyr Asn Asn Leu  
 370 375 380  
 Arg Ala Asp Tyr Asn Asn Leu Arg Ala Asp Tyr Asp Arg Leu Leu Gln  
 385 390 395 400  
 Asn Arg Ser Pro Leu Leu Glu Leu Ser Gln Asn Thr Thr Phe Lys Ile  
 405 410 415  
 Tyr His Lys Ala Tyr His Lys Ser Leu Pro Leu Leu Arg Ala Ile Arg  
 420 425 430  
 Arg Trp Val Lys Lys Leu Gly Leu  
 435 440

<210> 19  
 <211> 1664  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <223> H. pylori strain 948 FutA fucosyltransferase

<400> 19  
 ggatcccggc gtgaattact acctttcttg cttgcacagc tatgccgcag gcgatccctt 60  
 gcccatcccc actttcttat actttttaat agcgatacct tttgctctcg tgatcttggc 120  
 gtatttcaaa cgccatttga gtttgccata attgggttaa aggataaaaa tggtccagcc 180  
 cttactagac gctttcatag acagcaccga tttagatgaa acaaccata agccccatt 240  
 aaatgtagcc ctagccaatt ggtggccctt aaaaaatagc gaaaaaaaaag gattcagaga 300  
 cttcattttg catttcatcc taaaacaacg ctataaaaatc attctgcaca gcaaccctaa 360  
 tgaaccctca gatctagtct ttggcaatcc tttggaacaa gccagaaaaa tcttatctta 420  
 tcaaaacact aaacgagtggt tttacaccgg cgaaaatgaa gtgcctaatt tcaatctctt 480  
 tgattacgcc ataggctttg atgaattgga ttttaacgat cgctatttga gaatgccttt 540  
 gtattacgcc tatttgcatt ataaagccat gcttggttaat gacaccactt cgccctataa 600  
 actcaaagcc ctttataactt taaaaaaacc ttcccataaa tttaaagaaa accaccccaa 660  
 tttatgtgcg ctaatccata acgagagcga tccttggaaa agagggtttg ccagttttgt 720  
 cgcaagcaat cctaacgctc ccatacagaaa cgctttctat gacgctttaa atgctattga 780  
 gccagtggct agtggaggga gtgtgaaaaa cactctaggc tataagggtca aaaacaaaaa 840  
 cgaattttta agccaatata agttcaacct ctgttttgaa aactcacaag gctatggcta 900  
 tgtaaccgaa aaaatccttg atgcgtattt cagccacact atccctattt attgggggag 960  
 tcccagcgtg gcgaaagatt ttaaccctaa aagttttgtg aatgtgcatg atttcaacaa 1020  
 ctttgatgaa gcgattgatt atatcagata tttacacgcg caccaaaacg cttattttaga 1080  
 catgctttat gaaaaccctt taaacaccat tgatgggaaa gcgggttttt accaagattt 1140  
 gagttttgaa aagatcttag attttttcaa aaacattctt gaaaacgata cgatttatca 1200  
 ttgcaatgat gccattatt ctgctcttca tcgtgatttg aatgagccgt tagtgtctgt 1260  
 tgatgatttg agaagagatc atgatgattt gaggggttaat tatgatgatt tgagagttaa 1320  
 ttatgatgat ttgagagtta attatgatga tttgagagtt aattatgatg atttgagagt 1380  
 taattatgat gatttgagaa gagatcatga tgatttgaga agagatcatg aacgcctctt 1440  
 atcaaaggct acccctttat tggagctatc ccaaaacacc tcttttaaaa tctatcgcaa 1500  
 agcttatcaa aagtccttac ccttggttgc tgccataaaa acaattcaat cgcttcattg 1560  
 cttgagggca tgctcgcccc ttcagccacg catttgcacc cattagaaaag gaggggtttg 1620  
 cggaattcct gcagcccggg ggatcccccg ggctgcagga attc 1664

<210> 20  
 <211> 456  
 <212> PRT  
 <213> Helicobacter pylori

<220>

<223> H. pylori strain 948 FutA fucosyltransferase

<400> 20

Met	Phe	Gln	Pro	Leu	Leu	Asp	Ala	Phe	Ile	Asp	Ser	Thr	His	Leu	Asp		
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Glu	Thr	Thr	His	Lys	Pro	Pro	Leu	Asn	Val	Ala	Leu	Ala	Asn	Trp	Trp		
			20					25					30				
Pro	Leu	Lys	Asn	Ser	Glu	Lys	Lys	Gly	Phe	Arg	Asp	Phe	Ile	Leu	His		
		35					40					45					
Phe	Ile	Leu	Lys	Gln	Arg	Tyr	Lys	Ile	Ile	Leu	His	Ser	Asn	Pro	Asn		
	50					55					60						
Glu	Pro	Ser	Asp	Leu	Val	Phe	Gly	Asn	Pro	Leu	Glu	Gln	Ala	Arg	Lys		
65		-			70				75						80		
Ile	Leu	Ser	Tyr	Gln	Asn	Thr	Lys	Arg	Val	Phe	Tyr	Thr	Gly	Glu	Asn		
				85				90						95			
Glu	Val	Pro	Asn	Phe	Asn	Leu	Phe	Asp	Tyr	Ala	Ile	Gly	Phe	Asp	Glu		
			100					105					110				
Leu	Asp	Phe	Asn	Asp	Arg	Tyr	Leu	Arg	Met	Pro	Leu	Tyr	Tyr	Ala	Tyr		
		115					120					125					
Leu	His	Tyr	Lys	Ala	Met	Leu	Val	Asn	Asp	Thr	Thr	Ser	Pro	Tyr	Lys		
	130					135					140						
Leu	Lys	Ala	Leu	Tyr	Thr	Leu	Lys	Lys	Pro	Ser	His	Lys	Phe	Lys	Glu		
145					150					155					160		
Asn	His	Pro	Asn	Leu	Cys	Ala	Leu	Ile	His	Asn	Glu	Ser	Asp	Pro	Trp		
				165					170					175			
Lys	Arg	Gly	Phe	Ala	Ser	Phe	Val	Ala	Ser	Asn	Pro	Asn	Ala	Pro	Ile		
			180					185					190				
Arg	Asn	Ala	Phe	Tyr	Asp	Ala	Leu	Asn	Ala	Ile	Glu	Pro	Val	Ala	Ser		
	195						200					205					
Gly	Gly	Ser	Val	Lys	Asn	Thr	Leu	Gly	Tyr	Lys	Val	Lys	Asn	Lys	Asn		
	210					215					220						
Glu	Phe	Leu	Ser	Gln	Tyr	Lys	Phe	Asn	Leu	Cys	Phe	Glu	Asn	Ser	Gln		
225					230					235					240		
Gly	Tyr	Gly	Tyr	Val	Thr	Glu	Lys	Ile	Leu	Asp	Ala	Tyr	Phe	Ser	His		
				245					250					255			
Thr	Ile	Pro	Ile	Tyr	Trp	Gly	Ser	Pro	Ser	Val	Ala	Lys	Asp	Phe	Asn		
		260					265						270				
Pro	Lys	Ser	Phe	Val	Asn	Val	His	Asp	Phe	Asn	Asn	Phe	Asp	Glu	Ala		
		275					280					285					
Ile	Asp	Tyr	Ile	Arg	Tyr	Leu	His	Ala	His	Gln	Asn	Ala	Tyr	Leu	Asp		
	290					295					300						

Met Leu Tyr Glu Asn Pro Leu Asn Thr Ile Asp Gly Lys Ala Gly Phe  
305 310 315 320

Tyr Gln Asp Leu Ser Phe Glu Lys Ile Leu Asp Phe Phe Lys Asn Ile  
325 330 335

Leu Glu Asn Asp Thr Ile Tyr His Cys Asn Asp Ala His Tyr Ser Ala  
340 345 350

Leu His Arg Asp Leu Asn Glu Pro Leu Val Ser Val Asp Asp Leu Arg  
355 360 365

Arg Asp His Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn  
370 375 380

Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp  
385 390 395 400

Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Arg Asp His Asp Asp Leu  
405 410 415

Arg Arg Asp His Glu Arg Leu Leu Ser Lys Ala Thr Pro Leu Leu Glu  
420 425 430

Leu Ser Gln Asn Thr Ser Phe Lys Ile Tyr Arg Lys Ala Tyr Gln Lys  
435 440 445

Ser Leu Pro Leu Leu Arg Ala Ile  
450 455

<210> 21  
<211> 1895  
<212> DNA  
<213> Helicobacter pylori

<220>  
<223> H. pylori strain 955 FutA fucosyltransferase

<400> 21  
ggatcccagag cgaccaatca ttacagggat ttattaaatt tagatgtggc tttcagtaac 60  
acgctgatag tggaaaatgg tgccttaaac ggcttggtta cggggcatat gatgttttca 120  
cactctaaag gcgaaatgct tctcgcccta caacgcttgc taaatatcag tgaaacgagc 180  
acttttagttg tgggcgatgg agcgaatgac ttgagcatgt tcaaacatgc ccatattaaa 240  
atcgcttttca acgctaaaga ggtttttaaaa caacacgcca cgcattgcat caatgagcct 300  
gatttagccc taatcaagcc ttgtatttaa aaaatttttt ttgtaaaata ctcttttaaa 360  
ggataaagat gttccagccc ctattagatg ccttcataga aagcgcttca attaaaaaaa 420  
aattgcctct aaatctcccc cccctaaaaa atcgctgtgg cgaattgggt taacggcact 480  
aaagaatttta aagcgagcgt tctttatttc atcctaaaaa aacgctataa aatcattctg 540  
cacagcaacc ctaatgaacc ctcagatcta gtcttttgga atcctttgga acaagccaga 600  
aaaatcttat cttatcaaaa cactaaacga gtgttttaca ccggcgaaaa tgaagtgcct 660  
aatttcaatc tctttgatta cgccataggc tttgatgaat tggattttta cgatcgctat 720  
ttgagaatgc ctttgtatta cgcctatttg cattataaag ccatgcttgt taatgacacc 780  
acttcgcccct ataaactcaa agccctttat acttttaaaaa aaccttccca taaattttaa 840  
gaaaaccacc ccaatttatg tgcgctaata cataacgaga gcgatccttg gaaaagaggg 900  
tttgccagtt ttgtcgcaag caatcctaag gctcccata gaaacgctt ctatgacgct 960  
ttaaatgcta ttgagccagt ggctagtga gggagtgtga aaaacactct aggtataaag 1020  
gtcaaaaaca aaaacgaatt tttaagccaa tacaagttca acctctgttt tgaaaactca 1080  
caaggctatg gctatgtaac cgaaaaaatt ccttgatgcy tatttcagcc acactatccc 1140  
tattttattgg gggagtccca gcgtggcgaa agatttttaac cctaaaagtt ttgtgaatgt 1200  
gcatgatttc aacaactttg atgaagcgat tgattatatc agatatttac acgcgcacca 1260

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aaacgcttat ttagacatgc tttatgaaaa ccccttaaacc accattgatg ggaaagcggg 1320
tttttaccaa gatttgagtt ttgaaaagat cttagatttt ttcaaaaaca ttcttgaaaa 1380
cgatacgatt tatcattgca atgatgccca ttattctgct cttcatcgtg atttgaatga 1440
gccgtagtg tctgttgatg atttgagaag agatcatgat gatttgaggg ttaattatga 1500
tgatttgaga agagatcatg aacgcctctt atcaaaggct acccctcttt tggagctatc 1560
ccaaaacacc tcttttaaaa tctatcgcaa agcttatcaa aagtccttac ccttggtgcg 1620
tgccataagg aagtgggtta aaaaataagg cgtattttta gactgatgaa gaaattgaag 1680
cgctatttta aaatgcgcta acgcttcttt ttgagcgtg gggtttttga gcatgtcctc 1740
taaagcatgg gtgcttaaaa aatgttttgt ttttaaagac acgatgcgtc caaaggattc 1800
ttcttttagaa aggttttaaaa ggcgtttggg caaaatctcg ccaaatacca caatgacttt 1860
tgaagcgtg ttgtctaatt gccaggtcgg aattc 1895

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<210> 22
<211> 49
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:H. pylori
      strain 955 FutA fucosyltransferase coding
      sequence amino acid translation peptide

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<400> 22
Met Phe Lys His Ala His Ile Lys Ile Ala Phe Asn Ala Lys Glu Val
  1             5             10             15
Leu Lys Gln His Ala Thr His Cys Ile Asn Glu Pro Asp Leu Ala Leu
      20             25             30
Ile Lys Pro Leu Ile Phe Lys Ile Phe Phe Val Lys Tyr Ser Phe Lys
      35             40             45

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Gly

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<210> 23
<211> 6
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:H. pylori
      strain 955 FutA fucosyltransferase coding
      sequence amino acid translation peptide

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<400> 23
Arg Cys Ser Ser Pro Tyr
  1             5

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<210> 24
<211> 10
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:H. pylori
      strain 955 FutA fucosyltransferase coding
      sequence amino acid translation peptide

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<400> 24

Lys Ala Leu Gln Leu Lys Lys Asn Cys Leu  
1 5 10

<210> 25

<211> 227

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:H. pylori  
strain 955 FutA fucosyltransferase coding  
sequence amino acid translation peptide

<400> 25

Ile Ser Pro Pro Leu Lys Ile Ala Val Ala Asn Trp Phe Asn Gly Thr  
1 - 5 10 15

Lys Glu Phe Lys Ala Ser Val Leu Tyr Phe Ile Leu Lys Gln Arg Tyr  
20 25 30

Lys Ile Ile Leu His Ser Asn Pro Asn Glu Pro Ser Asp Leu Val Phe  
35 40 45

Gly Asn Pro Leu Glu Gln Ala Arg Lys Ile Leu Ser Tyr Gln Asn Thr  
50 55 60

Lys Arg Val Phe Tyr Thr Gly Glu Asn Glu Val Pro Asn Phe Asn Leu  
65 70 75 80

Phe Asp Tyr Ala Ile Gly Phe Asp Glu Leu Asp Phe Asn Asp Arg Tyr  
85 90 95

Leu Arg Met Pro Leu Tyr Tyr Ala Tyr Leu His Tyr Lys Ala Met Leu  
100 105 110

Val Asn Asp Thr Thr Ser Pro Tyr Lys Leu Lys Ala Leu Tyr Thr Leu  
115 120 125

Lys Lys Pro Ser His Lys Phe Lys Glu Asn His Pro Asn Leu Cys Ala  
130 135 140

Leu Ile His Asn Glu Ser Asp Pro Trp Lys Arg Gly Phe Ala Ser Phe  
145 150 155 160

Val Ala Ser Asn Pro Asn Ala Pro Ile Arg Asn Ala Phe Tyr Asp Ala  
165 170 175

Leu Asn Ala Ile Glu Pro Val Ala Ser Gly Gly Ser Val Lys Asn Thr  
180 185 190

Leu Gly Tyr Lys Val Lys Asn Lys Asn Glu Phe Leu Ser Gln Tyr Lys  
195 200 205

Phe Asn Leu Cys Phe Glu Asn Ser Gln Gly Tyr Gly Tyr Val Thr Glu  
210 215 220

Lys Ile Pro  
225

<210> 26  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:H. pylori  
strain 955 FutA fucosyltransferase coding  
sequence amino acid translation peptide

<400> 26  
Cys Val Phe Gln Pro His Tyr Pro Tyr Leu Leu Gly Glu Ser Gln Arg  
1 5 10 15

Gly Glu Arg Phe  
20

<210> 27  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:H. pylori  
strain 955 FutA fucosyltransferase coding  
sequence amino acid translation peptide

<400> 27  
Lys Phe Cys Glu Cys Ala  
1 5

<210> 28  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:H. pylori  
strain 955 FutA fucosyltransferase coding  
sequence amino acid translation peptide

<400> 28  
Phe Gln Gln Leu  
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<210> 29  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:H. pylori  
strain 955 FutA fucosyltransferase coding  
sequence amino acid translation peptide

<400> 29  
Leu Tyr Gln Ile Phe Thr Arg Ala Pro Lys Arg Leu Phe Arg His Ala  
1 5 10 15

Leu

<210> 30  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:H. pylori  
strain 955 FutA fucosyltransferase coding  
sequence amino acid translation peptide

<400> 30 -  
Lys Pro Leu Lys His His  
1 5

<210> 31  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:H. pylori  
strain 955 FutA fucosyltransferase coding  
sequence amino acid translation peptide

<400> 31  
Trp Glu Ser Gly Phe Leu Pro Arg Phe Glu Phe  
1 5 10

<210> 32  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:H. pylori  
strain 955 FutA fucosyltransferase coding  
sequence amino acid translation peptide

<400> 32  
Lys Asp Leu Arg Phe Phe Gln Lys His Ser  
1 5 10

<210> 33  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:H. pylori  
strain 955 FutA fucosyltransferase coding  
sequence amino acid translation peptide

<400> 33  
Lys Arg Tyr Asp Leu Ser Leu Gln  
1 5

<210> 34  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:H. pylori  
strain 955 FutA fucosyltransferase coding  
sequence amino acid translation peptide

<400> 34  
Cys Pro Leu Phe Cys Ser Ser Ser  
1 5

<210> 35  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:H. pylori  
strain 955 FutA fucosyltransferase coding  
sequence amino acid translation peptide

<400> 35  
Ala Val Ser Val Cys  
1 5

<210> 36  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:H. pylori  
strain 955 FutA fucosyltransferase coding  
sequence amino acid translation peptide

<400> 36  
Phe Glu Lys Arg Ser  
1 5

<210> 37  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:H. pylori  
strain 955 FutA fucosyltransferase coding  
sequence amino acid translation peptide



<400> 37

Thr Pro Leu Ile Lys Gly Tyr Pro Ser Phe Gly Ala Ile Pro Lys His  
1 5 10 15

Leu Phe

<210> 38

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:H. pylori  
strain 955 FutA fucosyltransferase coding  
sequence amino acid translation peptide

<400> 38 -

Asn Leu Ser Gln Ser Leu Ser Lys Val Leu Thr Leu Val Ala Cys His  
1 5 10 15

Lys Glu Val Gly  
20

<210> 39

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:H. pylori  
strain 955 FutA fucosyltransferase coding  
sequence amino acid translation peptide

<400> 39

Lys Ile Arg Arg Ile Leu Arg Leu Met Lys Lys Leu Lys Arg Tyr Phe  
1 5 10 15

Lys Met Arg

<210> 40

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:H. pylori  
strain 955 FutA fucosyltransferase coding  
sequence amino acid translation peptide

<400> 40

Arg Phe Phe Phe Glu Arg Gly Val Phe Glu His Val Leu  
1 5 10

<210> 41

<211> 4

<212> PRT

<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 955 FutA fucosyltransferase coding  
 sequence amino acid translation peptide  
  
 <400> 41  
 Ser Met Gly Ala  
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 <210> 42  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 955 FutA fucosyltransferase coding  
 sequence amino acid translation peptide  
  
 <400> 42  
 Lys Met Phe Cys Phe  
 1 5  
  
 <210> 43  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 955 FutA fucosyltransferase coding  
 sequence amino acid translation peptide  
  
 <400> 43  
 Arg His Asp Ala Ser Lys Gly Phe Phe Phe Arg Lys Val  
 1 5 10  
  
 <210> 44  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 955 FutA fucosyltransferase coding  
 sequence amino acid translation peptide  
  
 <400> 44  
 Lys Ala Phe Gly Gln Asn Leu Ala Lys Tyr His Asn Asp Phe  
 1 5 10  
  
 <210> 45  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 955 FutA fucosyltransferase coding  
 sequence amino acid translation peptide

<400> 45  
 Ser Ala Val Val  
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<210> 46  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 955 FutA fucosyltransferase coding  
 sequence amino acid translation peptide

<400> 46  
 Leu Pro Gly Arg Asn  
 1 5

<210> 47  
 <211> 1742  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <223> H. pylori strain 1218 FutA fucosyltransferase

<400> 47  
 ggatcctctg gcttgcacag ctatgccgca ggcgatccct tgcctatccc tactttctta 60  
 tacctttttg gtagcgatac ctttcgctct cgtgatcttg gcttatttca aacgccattt 120  
 gagtttgcct aaattgggtt aaaggataac catgttccaa cccctattag acgcttatat 180  
 agaaaagcgt tccattgaaa aaattacctc taaatctccc cccccctaa aaatcgctgt 240  
 ggcgaattgg tggggagatg aagagggtga agaatttaaa aagaacattc tttattttat 300  
 tctcagtcag cattacacaa tcacctcca ccaaaacccc aacgaaccct ccgatctcgt 360  
 ctttggcagt cctattggat cagccagaaa aatcttatcc tatcaaaacg caaaaagagt 420  
 gttttacacc ggtgaaaacg aatcgccata tttcaacctc tttgattacg ccataggcct 480  
 tgatgaatgg attttagaga tcgttattta agaatgcctt tatattatga tagactacac 540  
 cataaagccg agagcgtgaa tgacaccact tcgccttaca aactcaaacc tgacagcctt 600  
 tatgctttta aaaaaccctc ccatcatttt aaagaaaacc accccaattt atgcgcagta 660  
 gtgaacaatg agagcgatcc tttgaaaaga gggtttgcca gttttgtagc gagcaaccct 720  
 aacgctccta aaaggaatgc tttctatgac gcttttaaatt ctatagagcc agttattggg 780  
 ggaggggagc tgaaaaacac tttaggctat aacattaaaa acaagagcga gtttttaagc 840  
 caatacaaat tcaatctgtg ttttgaaaac tcacaaggct atggctatgt aactgaaaaa 900  
 atcattgacg cttacttttag ccataccatt cctattttatt gggggagtc tagcgtggca 960  
 caagatttta accctaagag ttttgatgat gtttgatgat ttaaagattt tgatgaagcg 1020  
 attgatcatg tgcgatactt gcacacgcac ccaaacgctt atttagacat gctttatgaa 1080  
 aaccctttta acacccttga tgggaaagct tactttccaa aatttgagtt ttaaaaaaat 1140  
 cctagatttt tttaaaacga tcttagaaaa cgacacgatt tatcacgata acccttttat 1200  
 tttttatcgt gatttgaatg agccgttaat atctattgat gatttgaggg ttaattatga 1260  
 tgatttgagg gttaattatg atgatttgag ggtaattat gatgatttga gggtaatta 1320  
 tgatgatttg agggtaatt atgatgattt gagggtaatt tatgatgatt tgaggggtta 1380  
 ttatgatgat ttgagggtta attatgatga tttgagggtt aattgtgatg atttgaggg 1440  
 taattatgat gatttgaggg ttaattatga gcggctctta caaaacgcct cgcctttatt 1500  
 agaactctct caaaacacca cttttaaaat ctatcgcaa gcttatcaa aatccttacc 1560  
 tttgttgcgt gcggcgagaa agttgattaa aaaattgggt ttgtaaaatt gggggtaatc 1620

aaaccccttg cgctatcatc gcagacgcca cttttctaaa accagcgata ttagccccta 1680  
 aaacaaaatt agtaggggtct ttaaactctt tagcggtttg agagacattc ttataagaat 1740  
 tc 1742

<210> 48  
 <211> 119  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 1218 FutA fucosyltransferase coding  
 sequence amino acid translation peptide

<400> 48  
 Met Phe Gln Pro Leu Leu Asp Ala Tyr Ile Glu Ser Ala Ser Ile Glu  
 1 - 5 10 15  
 Lys Ile Thr Ser Lys Ser Pro Pro Pro Leu Lys Ile Ala Val Ala Asn  
 20 25 30  
 Trp Trp Gly Asp Glu Glu Val Glu Glu Phe Lys Lys Asn Ile Leu Tyr  
 35 40 45  
 Phe Ile Leu Ser Gln His Tyr Thr Ile Thr Leu His Gln Asn Pro Asn  
 50 55 60  
 Glu Pro Ser Asp Leu Val Phe Gly Ser Pro Ile Gly Ser Ala Arg Lys  
 65 70 75 80  
 Ile Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn  
 85 90 95  
 Glu Ser Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu  
 100 105 110  
 Trp Ile Leu Glu Ile Val Ile  
 115

<210> 49  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 1218 FutA fucosyltransferase coding  
 sequence amino acid translation peptide

<400> 49  
 Glu Cys Leu Tyr Ile Met Ile Asp Tyr Thr Ile Lys Pro Arg Ala  
 1 5 10 15

<210> 50  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 1218 FutA fucosyltransferase coding  
 sequence amino acid translation peptide

<400> 50  
 Met Thr Pro Leu Arg Leu Thr Asn Ser Asn Leu Thr Ala Phe Met Leu  
           1                  5                  10                  15

<210> 51  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 1218 FutA fucosyltransferase coding  
 sequence amino acid translation peptide

<400> 51  
 Lys Asn Pro Pro Ile Ile Leu Lys Lys Thr Thr Pro Ile Tyr Ala Gln  
           1                  5                  10                  15

<210> 52  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 1218 FutA fucosyltransferase coding  
 sequence amino acid translation peptide

<400> 52  
 Thr Met Arg Ala Ile Leu  
           1                  5

<210> 53  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 1218 FutA fucosyltransferase coding  
 sequence amino acid translation peptide

<400> 53  
 Lys Glu Gly Leu Arg Val Leu  
           1                  5

<210> 54  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 1218 FutA fucosyltransferase coding  
 sequence amino acid translation peptide

<400> 54  
 Arg Ala Thr Leu Thr Leu Leu Lys Gly Met Leu Ser Met Thr Leu  
 1 5 10 15

<210> 55  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 1218 FutA fucosyltransferase coding  
 sequence amino acid translation peptide

<400> 55  
 Ser Gln Leu Leu Gly Glu Gly Ala  
 1 5

<210> 56  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 1218 FutA fucosyltransferase coding  
 sequence amino acid translation peptide

<400> 56  
 Ala Ile Thr Leu Lys Thr Arg Ala Ser Phe  
 1 5 10

<210> 57  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 1218 FutA fucosyltransferase coding  
 sequence amino acid translation peptide

<400> 57  
 Ala Asn Thr Asn Ser Ile Cys Val Leu Lys Thr His Lys Ala Met Ala  
 1 5 10 15

Met

<210> 58  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 1218 FutA fucosyltransferase coding  
 sequence amino acid translation peptide

<400> 58  
 Leu Lys Lys Ser Leu Thr Leu Thr Leu Ala Ile Pro Phe Leu Phe Ile  
 1 5 10 15  
 Gly Gly Val Leu Ala Trp His Lys Ile Leu Thr Leu Arg Val Leu  
 20 25 30

<210> 59  
 <211> 25  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 1218 FutA fucosyltransferase coding  
 sequence amino acid translation peptide

<400> 59  
 Met Phe Val Ile Leu Lys Ile Leu Met Lys Arg Leu Ile Met Cys Asp  
 1 5 10 15  
 Thr Cys Thr Arg Thr Gln Thr Leu Ile  
 20 25

<210> 60  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 1218 FutA fucosyltransferase coding  
 sequence amino acid translation peptide

<400> 60  
 Thr Cys Phe Met Lys Thr Leu  
 1 5

<210> 61  
 <211> 171  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
 strain 1218 FutA fucosyltransferase coding  
 sequence amino acid translation peptide

<400> 61  
 Thr Pro Leu Met Gly Lys Leu Thr Phe Gln Asn Leu Ser Phe Lys Lys  
 1 5 10 15

Ile Leu Asp Phe Phe Lys Thr Ile Leu Glu Asn Asp Thr Ile Tyr His  
                   20                                  25                                  30  
 Asp Asn Pro Phe Ile Phe Tyr Arg Asp Leu Asn Glu Pro Leu Ile Ser  
                   35                                  40                                  45  
 Ile Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp  
                   50                                  55                                  60  
 Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu  
                   65                                  70                                  75                                  80  
 Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val  
                                   85                                  90                                  95  
 Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Cys  
                   100                                  105                                  110  
 Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Glu Arg  
                   115                                  120                                  125  
 Leu Leu Gln Asn Ala Ser Pro Leu Leu Glu Leu Ser Gln Asn Thr Thr  
                   130                                  135                                  140  
 Phe Lys Ile Tyr Arg Lys Ala Tyr Gln Lys Ser Leu Pro Leu Leu Arg  
                   145                                  150                                  155                                  160  
 Ala Ala Arg Lys Leu Ile Lys Lys Leu Gly Leu  
                                   165                                  170

<210> 62  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
           strain 1218 FutA fucosyltransferase coding  
           sequence amino acid translation peptide

<400> 62  
 Ser Asn Pro Leu Arg Tyr His Arg Arg Arg His Leu Ser Lys Thr Ser  
       1                                  5                                  10                                  15

Asp Ile Ser Pro  
                   20

<210> 63  
 <211> 35  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:H. pylori  
           strain 1218 FutA fucosyltransferase coding  
           sequence amino acid translation peptide



<400> 63

Asn Lys Ile Ser Arg Val Phe Lys Leu Phe Ser Gly Leu Arg Asp Ile  
1 5 10 15

Leu Ile Arg Ile Arg Tyr Gln Ala Tyr Arg Tyr Arg Arg Pro Arg Gly  
20 25 30

Gly Ala Arg  
35

<210> 64

<211> 231

<212> PRT

<213> Helicobacter pylori

<220>

<223> H. pylori strain 1182 FutB fucosyltransferase  
catalytic domain conserved region positions 23-305

<400> 64

Pro Pro Pro Leu Lys Ile Ala Val Ala Asn Trp Trp Gly Asp Glu Glu  
1 5 10 15

Val Glu Glu Phe Lys Lys Asn Ile Leu Tyr Phe Ile Leu Ser Gln His  
20 25 30

Tyr Thr Ile Thr Leu His Gln Asn Pro Asn Glu Pro Ser Asp Leu Val  
35 40 45

Phe Gly Ser Pro Ile Gly Ser Ala Arg Lys Ile Leu Ser Tyr Gln Asn  
50 55 60

Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn Glu Ser Pro Asn Phe Asn  
65 70 75 80

Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu Leu Asp Phe Arg Asp Arg  
85 90 95

Tyr Leu Arg Met Pro Leu Tyr Tyr Asp Arg Leu His His Lys Ala Glu  
100 105 110

Ser Val Asn Asp Thr Thr Ser Pro Tyr Lys Leu Lys Pro Asp Ser Leu  
115 120 125

Tyr Ala Leu Lys Lys Pro Ser His His Phe Lys Glu Asn His Pro Asn  
130 135 140

Leu Cys Ala Val Val Asn Asn Glu Ser Asp Pro Leu Lys Arg Gly Phe  
145 150 155 160

Ala Ser Phe Val Ala Ser Asn Pro Asn Ala Pro Lys Arg Asn Ala Phe  
165 170 175

Tyr Asp Val Leu Asn Ser Ile Glu Pro Val Ile Gly Gly Gly Ser Val  
180 185 190

Lys Asn Thr Leu Gly Tyr Asn Ile Lys Asn Lys Ser Glu Phe Leu Ser  
195 200 205

Gln Tyr Lys Phe Asn Leu Cys Phe Glu Asn Ser Gln Gly Tyr Gly Tyr  
 210 215 220

Val Thr Glu Lys Ile Ile Asp  
 225 230

<210> 65  
 <211> 291  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial  
 Sequence:glycosyltransferase family 10  
 fucosyltransferase consensus sequence pfam00852  
 positions 11-301

<400> 65  
 Thr Val Pro Leu Leu Leu Ala Ile Tyr Thr Trp Trp Ser Leu Ile Glu  
 1 5 10 15  
 Tyr Lys Glu Trp Lys Lys Ser Pro Ile Tyr Phe Ile Gly Ser Gln Ala  
 20 25 30  
 Pro Gln Pro Pro Leu Arg Ile Leu Leu Trp Thr Trp Pro Phe Asn Gly  
 35 40 45  
 Asn Pro Leu Ala Leu Ser Asp Cys Pro Leu Ser Tyr Gln Asn Thr Ala  
 50 55 60  
 Arg Cys Arg Leu Thr Ala Asn Arg Ser Pro Leu Glu Ser Ala Asp Ala  
 65 70 75 80  
 Val Leu Phe His His Arg Asp Leu Ser Lys Gly Phe Pro Asp Leu Pro  
 85 90 95  
 Pro Ser Pro Arg Pro Pro Gly Gln Pro Trp Val Trp Ala Ser Met Glu  
 100 105 110  
 Ser Pro Ser Asn Ser Gly Leu Asn Asp Leu Arg Asp Gly Tyr Phe Asn  
 115 120 125  
 Trp Thr Leu Ser Tyr Arg Ala Asp Ser Asp Ala Phe His Pro Tyr Gly  
 130 135 140  
 Tyr Leu Glu Pro Arg Leu Ser Gln Val Val Asn Ala Pro Leu Leu Ser  
 145 150 155 160  
 Ala Lys Arg Lys Gly Ala Ala Trp Val Val Ser Asn Cys Asn Thr Arg  
 165 170 175  
 Ser Lys Arg Glu Arg Phe Tyr Lys Gln Leu Asn Lys His Leu Gln Val  
 180 185 190  
 Asp Val Gly Gly Arg Val Ala Asn Pro Leu Pro Leu Lys Val Gly Cys  
 195 200 205  
 Leu Val Glu Thr Leu Ser Gln Tyr Lys Phe Tyr Leu Ala Phe Glu Asn  
 210 215 220

Ser Gln His Tyr Asp Tyr Val Thr Glu Lys Leu Trp Lys Asn Ala Leu  
 225 230 235 240

Gln Ala Gly Thr Ile Pro Val Val Leu Gly Pro Arg Ala Val Tyr Glu  
 245 250 255

Asp Phe Val Pro Pro Lys Ser Phe Ile His Val Asp Asp Phe Lys Ser  
 260 265 270

Pro Lys Glu Leu Ala Asp Tyr Leu Leu Tyr Leu Asp Thr Asn Pro Thr  
 275 280 285

Ala Tyr Ser  
 290

<210> 66  
 <211> 391 -  
 <212> PRT  
 <213> Helicobacter pylori

<220>  
 <223> H. pylori strain 1111 FutA fucosyltransferase  
 catalytic domain conserved region positions 27-417

<400> 66  
 Ile Ala Val Ala Asn Trp Trp Gly Asp Glu Glu Ile Lys Lys Phe Lys  
 1 5 10 15

Lys Ser Val Leu Tyr Phe Ile Leu Ser Gln His Tyr Thr Ile Thr Leu  
 20 25 30

His Arg Asn Pro Asp Lys Pro Ala Asp Ile Val Phe Gly Asn Pro Leu  
 35 40 45

Gly Ser Ala Arg Lys Ile Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe  
 50 55 60

Tyr Thr Gly Glu Asn Glu Val Pro Asn Phe Asn Leu Phe Asp Tyr Ala  
 65 70 75 80

Ile Gly Phe Asp Glu Leu Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro  
 85 90 95

Leu Tyr Tyr Ala Tyr Leu His Tyr Lys Ala Glu Leu Val Asn Asp Thr  
 100 105 110

Thr Ser Pro Tyr Lys Leu Gln Pro Asp Ser Leu Tyr Ala Leu Lys Lys  
 115 120 125

Pro Ser His His Phe Lys Glu Asn His Pro Asn Leu Cys Ala Val Val  
 130 135 140

Asn Asn Glu Ser Asp Pro Leu Lys Arg Gly Phe Ala Ser Phe Val Ala  
 145 150 155 160

Ser Asn Pro Asn Ala Pro Arg Arg Asn Ala Phe Tyr Glu Ala Leu Asn  
 165 170 175

Ala Ile Glu Pro Val Ala Gly Gly Gly Ser Val Lys Asn Thr Leu Gly  
 180 185 190

Tyr Asn Val Lys Asn Lys Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn  
 195 200 205  
 Leu Cys Phe Glu Asn Thr Gln Gly Tyr Gly Tyr Val Thr Glu Lys Ile  
 210 215 220  
 Ile Asp Ala Tyr Phe Ser His Thr Ile Pro Ile Tyr Trp Gly Ser Pro  
 225 230 235 240  
 Ser Val Ala Lys Asp Phe Asn Pro Lys Ser Phe Val Asn Val His Asp  
 245 250 255  
 Phe Asn Asn Phe Asp Glu Ala Ile Asp Tyr Ile Arg Tyr Leu His Thr  
 260 265 270  
 His Pro Asn Ala Tyr Leu Asp Met His Tyr Glu Asn Pro Leu Asn Thr  
 275 280 285  
 Ile Asp Gly Lys Ala Tyr Phe Tyr Gln Asn Leu Ser Phe Lys Lys Ile  
 290 295 300  
 Leu Asp Phe Phe Lys Thr Ile Leu Glu Asn Asp Thr Ile Tyr His Asp  
 305 310 315 320  
 Asn Pro Phe Ile Phe Tyr Arg Asp Leu Asn Glu Pro Ser Val Ser Ile  
 325 330 335  
 Asp Gly Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp  
 340 345 350  
 Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Glu Arg Leu Leu  
 355 360 365  
 Gln Asn Ala Ser Pro Leu Leu Glu Leu Ser Gln Asn Thr Thr Phe Lys  
 370 375 380  
 Ile Tyr Arg Lys Ala Tyr Gln  
 385 390

<210> 67  
 <211> 336  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial  
 Sequence:glycosyltransferase family 10  
 fucosyltransferase consensus sequence pfam00852  
 positions 16-351

<400> 67  
 Leu Ala Ile Tyr Thr Trp Trp Ser Leu Ile Glu Tyr Lys Glu Trp Lys  
 1 5 10 15  
 Lys Ser Pro Ile Tyr Phe Ile Gly Ser Gln Ala Pro Gln Pro Pro Leu  
 20 25 30  
 Arg Ile Leu Leu Trp Thr Trp Pro Phe Asn Gly Asn Pro Leu Ala Leu  
 35 40 45

Ser Asp Cys Pro Leu Ser Tyr Gln Asn Thr Ala Arg Cys Arg Leu Thr  
 50 55 60  
 Ala Asn Arg Ser Pro Leu Glu Ser Ala Asp Ala Val Leu Phe His His  
 65 70 75 80  
 Arg Asp Leu Ser Lys Gly Phe Pro Asp Leu Pro Pro Ser Pro Arg Pro  
 85 90 95  
 Pro Gly Gln Pro Trp Val Trp Ala Ser Met Glu Ser Pro Ser Asn Ser  
 100 105 110  
 Gly Leu Asn Asp Leu Arg Asp Gly Tyr Phe Asn Trp Thr Leu Ser Tyr  
 115 120 125  
 Arg Ala Asp Ser Asp Ala Phe His Pro Tyr Gly Tyr Leu Glu Pro Arg  
 130 135 140  
 Leu Ser Gln Val Val Asn Ala Pro Leu Leu Ser Ala Lys Arg Lys Gly  
 145 150 155 160  
 Ala Ala Trp Val Val Ser Asn Cys Asn Thr Arg Ser Lys Arg Glu Arg  
 165 170 175  
 Phe Tyr Lys Gln Leu Asn Lys His Leu Gln Val Asp Val Gly Gly Arg  
 180 185 190  
 Val Ala Asn Pro Leu Pro Leu Lys Val Gly Cys Leu Val Glu Thr Leu  
 195 200 205  
 Ser Gln Tyr Lys Phe Tyr Leu Ala Phe Glu Asn Ser Gln His Tyr Asp  
 210 215 220  
 Tyr Val Thr Glu Lys Leu Trp Lys Asn Ala Leu Gln Ala Gly Thr Ile  
 225 230 235 240  
 Pro Val Val Leu Gly Pro Arg Ala Val Tyr Glu Asp Phe Val Pro Pro  
 245 250 255  
 Lys Ser Phe Ile His Val Asp Asp Phe Lys Ser Pro Lys Glu Leu Ala  
 260 265 270  
 Asp Tyr Leu Leu Tyr Leu Asp Thr Asn Pro Thr Ala Tyr Ser Glu Tyr  
 275 280 285  
 Phe Glu Trp Arg Tyr Asp Leu Arg Val Arg Leu Phe Ser Trp Asp Ala  
 290 295 300  
 Leu Arg Tyr Asp Glu Gly Phe Cys Arg Val Cys Arg Leu Leu Gln Asn  
 305 310 315 320  
 Ala Pro Asp Arg Tyr Lys Thr Tyr Pro Asn Ile Ala Lys Trp Phe Gln  
 325 330 335

<210> 68

<211> 377

<212> PRT

<213> Helicobacter pylori

<220>

<223> H. pylori strain 1218 FutB fucosyltransferase  
catalytic domain conserved region positions 23-399

<400> 68

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Pro Pro Pro Leu Lys Ile Ala Val Ala Asn Trp Trp Gly Asp Glu Glu
  1           5           10           15

Val Glu Glu Phe Lys Lys Asn Ile Leu Tyr Phe Ile Leu Ser Gln His
  20           25           30

Tyr Thr Ile Thr Leu His Gln Asn Pro Asn Glu Pro Ser Asp Leu Val
  35           40           45

Phe Gly Ser Pro Ile Gly Ser Ala Arg Lys Ile Leu Ser Tyr Gln Asn
  50           55           60

Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn Glu Ser Pro Asn Phe Asn
  65           70           75           80

Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu Leu Asp Phe Arg Asp Arg
  85           90           95

Tyr Leu Arg Met Pro Leu Tyr Tyr Asp Arg Leu His His Lys Ala Glu
 100          105          110

Ser Val Asn Asp Thr Thr Ser Pro Tyr Lys Leu Lys Pro Asp Ser Leu
 115          120          125

Tyr Ala Leu Lys Lys Pro Ser His His Phe Lys Glu Asn His Pro Asn
 130          135          140

Leu Cys Ala Val Val Asn Asn Glu Ser Asp Pro Leu Lys Arg Gly Phe
 145          150          155          160

Ala Ser Phe Val Ala Ser Asn Pro Asn Ala Pro Lys Arg Asn Ala Phe
 165          170          175

Tyr Asp Ala Leu Asn Ser Ile Glu Pro Val Ile Gly Gly Gly Ser Val
 180          185          190

Lys Asn Thr Leu Gly Tyr Asn Ile Lys Asn Lys Ser Glu Phe Leu Ser
 195          200          205

Gln Tyr Lys Phe Asn Leu Cys Phe Glu Asn Ser Gln Gly Tyr Gly Tyr
 210          215          220

Val Thr Glu Lys Ile Ile Asp Ala Tyr Phe Ser His Thr Ile Pro Ile
 225          230          235          240

Tyr Trp Gly Ser Pro Ser Val Ala Gln Asp Phe Asn Pro Lys Ser Phe
 245          250          255

Val Asn Val Cys Asp Phe Lys Asp Phe Asp Glu Ala Ile Asp His Val
 260          265          270

Arg Tyr Leu His Thr His Pro Asn Ala Tyr Leu Asp Met Leu Tyr Glu
 275          280          285

Asn Pro Leu Asn Thr Leu Asp Gly Lys Ala Tyr Phe Tyr Gln Asn Leu
 290          295          300
```

Ser Phe Lys Lys Ile Leu Asp Phe Phe Lys Thr Ile Leu Glu Asn Asp  
305 310 315 320

Thr Ile Tyr His Asp Asn Pro Phe Ile Phe Tyr Arg Asp Leu Asn Glu  
325 330 335

Pro Leu Ile Ser Ile Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg  
340 345 350

Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn  
355 360 365

Tyr Asp Asp Leu Arg Val Asn Tyr Asp  
370 375

<210> 69

<211> 341-

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial

Sequence:glycosyltransferase family 10

fucosyltransferase consensus sequence pfam00852

positions 11-351

<400> 69

Thr Val Pro Leu Leu Leu Ala Ile Tyr Thr Trp Trp Ser Leu Ile Glu  
1 5 10 15

Tyr Lys Glu Trp Lys Lys Ser Pro Ile Tyr Phe Ile Gly Ser Gln Ala  
20 25 30

Pro Gln Pro Pro Leu Arg Ile Leu Leu Trp Thr Trp Pro Phe Asn Gly  
35 40 45

Asn Pro Leu Ala Leu Ser Asp Cys Pro Leu Ser Tyr Gln Asn Thr Ala  
50 55 60

Arg Cys Arg Leu Thr Ala Asn Arg Ser Pro Leu Glu Ser Ala Asp Ala  
65 70 75 80

Val Leu Phe His His Arg Asp Leu Ser Lys Gly Phe Pro Asp Leu Pro  
85 90 95

Pro Ser Pro Arg Pro Pro Gly Gln Pro Trp Val Trp Ala Ser Met Glu  
100 105 110

Ser Pro Ser Asn Ser Gly Leu Asn Asp Leu Arg Asp Gly Tyr Phe Asn  
115 120 125

Trp Thr Leu Ser Tyr Arg Ala Asp Ser Asp Ala Phe His Pro Tyr Gly  
130 135 140

Tyr Leu Glu Pro Arg Leu Ser Gln Val Val Asn Ala Pro Leu Leu Ser  
145 150 155 160

Ala Lys Arg Lys Gly Ala Ala Trp Val Val Ser Asn Cys Asn Thr Arg  
165 170 175

Ser Lys Arg Glu Arg Phe Tyr Lys Gln Leu Asn Lys His Leu Gln Val  
 180 185 190  
 Asp Val Gly Gly Arg Val Ala Asn Pro Leu Pro Leu Lys Val Gly Cys  
 195 200 205  
 Leu Val Glu Thr Leu Ser Gln Tyr Lys Phe Tyr Leu Ala Phe Glu Asn  
 210 215 220  
 Ser Gln His Tyr Asp Tyr Val Thr Glu Lys Leu Trp Lys Asn Ala Leu  
 225 230 235 240  
 Gln Ala Gly Thr Ile Pro Val Val Leu Gly Pro Arg Ala Val Tyr Glu  
 245 250 255  
 Asp Phe Val Pro Pro Lys Ser Phe Ile His Val Asp Asp Phe Lys Ser  
 260 265 270  
 Pro Lys Glu Leu Ala Asp Tyr Leu Leu Tyr Leu Asp Thr Asn Pro Thr  
 275 280 285  
 Ala Tyr Ser Glu Tyr Phe Glu Trp Arg Tyr Asp Leu Arg Val Arg Leu  
 290 295 300  
 Phe Ser Trp Asp Ala Leu Arg Tyr Asp Glu Gly Phe Cys Arg Val Cys  
 305 310 315 320  
 Arg Leu Leu Gln Asn Ala Pro Asp Arg Tyr Lys Thr Tyr Pro Asn Ile  
 325 330 335  
 Ala Lys Trp Phe Gln  
 340

<210> 70  
 <211> 256  
 <212> PRT  
 <213> Helicobacter pylori

<220>  
 <223> H. pylori strain 19C2 FutB fucosyltransferase  
 catalytic domain conserved region positions 22-277

<400> 70  
 Pro Pro Leu Asn Ile Ala Leu Ala Asn Trp Trp Pro Leu Asp Lys Arg  
 1 5 10 15  
 Glu Ser Lys Gly Phe Arg Lys Lys Phe Ile Leu His Phe Ile Leu Ser  
 20 25 30  
 Gln His Tyr Thr Ile Ala Leu His Arg Asn Pro Asp Lys Pro Ala Asp  
 35 40 45  
 Ile Val Phe Gly Asn Pro Leu Gly Ser Ala Arg Lys Ile Leu Ser Tyr  
 50 55 60  
 Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn Glu Val Pro Asn  
 65 70 75 80  
 Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu Leu Asp Phe Arg  
 85 90 95



Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Asp Arg Leu His His Lys  
 100 105 110  
 Ala Glu Ser Val Asn Asp Thr Thr Ala Pro Tyr Lys Ile Lys Ser Asp  
 115 120 125  
 Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His Phe Lys Glu Asn His  
 130 135 140  
 Pro His Leu Cys Ala Leu Ile Asn Asn Glu Ile Asp Pro Leu Lys Arg  
 145 150 155 160  
 Gly Phe Ala Ser Phe Val Ala Ser Asn Pro Asn Ala Pro Ile Arg Asn  
 165 170 175  
 Ala Phe Tyr Glu Ala Leu Asn Ser Ile Glu Pro Val Thr Gly Gly Gly  
 180 185 190  
 Ser Val Arg Asn Thr Leu Gly Tyr Asn Val Lys Asn Lys Asn Glu Phe  
 195 200 205  
 Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu Asn Thr Gln Gly Tyr  
 210 215 220  
 Gly Tyr Val Thr Glu Lys Ile Ile Asp Ala Tyr Phe Ser His Thr Ile  
 225 230 235 240  
 Pro Ile Tyr Trp Gly Gly Val Pro Ser Val Ala Lys Asp Phe Asn Pro  
 245 250 255

<210> 71  
 <211> 259  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial  
 Sequence:glycosyltransferase family 10  
 fucosyltransferase consensus sequence pfam00852  
 positions 12-270

<400> 71  
 Val Pro Leu Leu Leu Ala Ile Tyr Thr Trp Trp Ser Leu Ile Glu Tyr  
 1 5 10 15  
 Lys Glu Trp Lys Lys Ser Pro Ile Tyr Phe Ile Gly Ser Gln Ala Pro  
 20 25 30  
 Gln Pro Pro Leu Arg Ile Leu Leu Trp Thr Trp Pro Phe Asn Gly Asn  
 35 40 45  
 Pro Leu Ala Leu Ser Asp Cys Pro Leu Ser Tyr Gln Asn Thr Ala Arg  
 50 55 60  
 Cys Arg Leu Thr Ala Asn Arg Ser Pro Leu Glu Ser Ala Asp Ala Val  
 65 70 75 80  
 Leu Phe His His Arg Asp Leu Ser Lys Gly Phe Pro Asp Leu Pro Pro  
 85 90 95

Ser Pro Arg Pro Pro Gly Gln Pro Trp Val Trp Ala Ser Met Glu Ser  
 100 105 110  
 Pro Ser Asn Ser Gly Leu Asn Asp Leu Arg Asp Gly Tyr Phe Asn Trp  
 115 120 125  
 Thr Leu Ser Tyr Arg Ala Asp Ser Asp Ala Phe His Pro Tyr Gly Tyr  
 130 135 140  
 Leu Glu Pro Arg Leu Ser Gln Val Val Asn Ala Pro Leu Leu Ser Ala  
 145 150 155 160  
 Lys Arg Lys Gly Ala Ala Trp Val Val Ser Asn Cys Asn Thr Arg Ser  
 165 170 175  
 Lys Arg Glu Arg Phe Tyr Lys Gln Leu Asn Lys His Leu Gln Val Asp  
 180 185 190  
 Val Gly Gly Arg Val Ala Asn Pro Leu Pro Leu Lys Val Gly Cys Leu  
 195 200 205  
 Val Glu Thr Leu Ser Gln Tyr Lys Phe Tyr Leu Ala Phe Glu Asn Ser  
 210 215 220  
 Gln His Tyr Asp Tyr Val Thr Glu Lys Leu Trp Lys Asn Ala Leu Gln  
 225 230 235 240  
 Ala Gly Thr Ile Pro Val Val Leu Gly Pro Arg Ala Val Tyr Glu Asp  
 245 250 255  
 Phe Val Pro

<210> 72  
 <211> 245  
 <212> PRT  
 <213> Helicobacter pylori

<220>  
 <223> H. pylori strain 1111 FutA fucosyltransferase  
 positions 1-245 (1111FutA.pep)

<400> 72  
 Met Phe Gln Pro Leu Leu Asp Ala Phe Ile Glu Ser Ala Pro Leu Lys  
 1 5 10 15  
 Lys Trp Pro Leu Asn Leu Pro Pro Leu Lys Ile Ala Val Ala Asn Trp  
 20 25 30  
 Trp Gly Asp Glu Glu Ile Lys Lys Phe Lys Lys Ser Val Leu Tyr Phe  
 35 40 45  
 Ile Leu Ser Gln His Tyr Thr Ile Thr Leu His Arg Asn Pro Asp Lys  
 50 55 60  
 Pro Ala Asp Ile Val Phe Gly Asn Pro Leu Gly Ser Ala Arg Lys Ile  
 65 70 75 80  
 Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn Glu  
 85 90 95

Val Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu Leu  
 100 105 110  
 Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Ala Tyr Leu  
 115 120 125  
 His Tyr Lys Ala Glu Leu Val Asn Asp Thr Thr Ser Pro Tyr Lys Leu  
 130 135 140  
 Gln Pro Asp Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His Phe Lys  
 145 150 155 160  
 Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asn Glu Ser Asp Pro  
 165 170 175  
 Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Pro Asn Ala Pro  
 180 185 190  
 Arg Arg Asn Ala Phe Tyr Glu Ala Leu Asn Ala Ile Glu Pro Val Ala  
 195 200 205  
 Gly Gly Gly Ser Val Lys Asn Thr Leu Gly Tyr Asn Val Lys Asn Lys  
 210 215 220  
 Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu Asn Thr  
 225 230 235 240  
 Gln Gly Tyr Gly Tyr  
 245

<210> 73

<211> 247

<212> PRT

<213> *Helicobacter pylori*

<220>

<223> *H. pylori* strain 26695 FutA fucosyltransferase  
 positions 1-247 (26695A.pep)

<400> 73

Met Phe Gln Pro Leu Leu Asp Ala Phe Ile Glu Ser Ala Ser Ile Glu  
 1 5 10 15  
 Lys Met Ala Ser Lys Ser Pro Pro Pro Leu Lys Ile Ala Val Ala  
 20 25 30  
 Asn Trp Trp Gly Asp Glu Glu Ile Lys Glu Phe Lys Lys Ser Val Leu  
 35 40 45  
 Tyr Phe Ile Leu Ser Gln Arg Tyr Ala Ile Thr Leu His Gln Asn Pro  
 50 55 60  
 Asn Glu Phe Ser Asp Leu Val Phe Ser Asn Pro Leu Gly Ala Ala Arg  
 65 70 75 80  
 Lys Ile Leu Ser Tyr Gln Asn Thr Lys Arg Val Phe Tyr Thr Gly Glu  
 85 90 95  
 Asn Glu Ser Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp  
 100 105 110

Glu Leu Asp Phe Asn Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Ala  
 115 120 125  
 His Leu His Tyr Lys Ala Glu Leu Val Asn Asp Thr Thr Ala Pro Tyr  
 130 135 140  
 Lys Leu Lys Asp Asn Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His  
 145 150 155 160  
 Phe Lys Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asp Glu Ser  
 165 170 175  
 Asp Leu Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Ala Asn  
 180 185 190  
 Ala Pro Met Arg Asn Ala Phe Tyr Asp Ala Leu Asn Ser Ile Glu Pro  
 195 200 205  
 Val Thr Gly Gly Gly Ser Val Arg Asn Thr Leu Gly Tyr Lys Val Gly  
 210 215 220  
 Asn Lys Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu  
 225 230 235 240  
 Asn Ser Gln Gly Tyr Gly Tyr  
 245

<210> 74

<211> 246

<212> PRT

<213> Helicobacter pylori

<220>

<223> H. pylori strain 1182 FutB fucosyltransferase  
 positions 1-246 (1182B.pep)

<400> 74

Met Phe Gln Pro Leu Leu Asp Ala Tyr Ile Glu Ser Ala Ser Ile Glu  
 1 5 10 15  
 Lys Ile Thr Ser Lys Ser Pro Pro Pro Leu Lys Ile Ala Val Ala Asn  
 20 25 30  
 Trp Trp Gly Asp Glu Glu Val Glu Glu Phe Lys Lys Asn Ile Leu Tyr  
 35 40 45  
 Phe Ile Leu Ser Gln His Tyr Thr Ile Thr Leu His Gln Asn Pro Asn  
 50 55 60  
 Glu Pro Ser Asp Leu Val Phe Gly Ser Pro Ile Gly Ser Ala Arg Lys  
 65 70 75 80  
 Ile Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn  
 85 90 95  
 Glu Ser Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu  
 100 105 110  
 Leu Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Asp Arg  
 115 120 125

Leu His His Lys Ala Glu Ser Val Asn Asp Thr Thr Ser Pro Tyr Lys  
 130 135 140  
 Leu Lys Pro Asp Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His Phe  
 145 150 155 160  
 Lys Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asn Glu Ser Asp  
 165 170 175  
 Pro Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Pro Asn Ala  
 180 185 190  
 Pro Lys Arg Asn Ala Phe Tyr Asp Val Leu Asn Ser Ile Glu Pro Val  
 195 200 205  
 Ile Gly Gly Gly Ser Val Lys Asn Thr Leu Gly Tyr Asn Ile Lys Asn  
 210 215 220  
 Lys Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu Asn  
 225 230 235 240  
 Ser Gln Gly Tyr Gly Tyr  
 245

<210> 75  
 <211> 246  
 <212> PRT  
 <213> *Helicobacter pylori*

<220>  
 <223> *H. pylori* strain 1218 FutB fucosyltransferase  
 positions 1-246 (1218B.pep)

<400> 75  
 Met Phe Gln Pro Leu Leu Asp Ala Tyr Ile Glu Ser Ala Ser Ile Glu  
 1 5 10 15  
 Lys Ile Thr Ser Lys Ser Pro Pro Pro Leu Lys Ile Ala Val Ala Asn  
 20 25 30  
 Trp Trp Gly Asp Glu Glu Val Glu Glu Phe Lys Lys Asn Ile Leu Tyr  
 35 40 45  
 Phe Ile Leu Ser Gln His Tyr Thr Ile Thr Leu His Gln Asn Pro Asn  
 50 55 60  
 Glu Pro Ser Asp Leu Val Phe Gly Ser Pro Ile Gly Ser Ala Arg Lys  
 65 70 75 80  
 Ile Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn  
 85 90 95  
 Glu Ser Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu  
 100 105 110  
 Leu Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Asp Arg  
 115 120 125  
 Leu His His Lys Ala Glu Ser Val Asn Asp Thr Thr Ser Pro Tyr Lys  
 130 135 140

Leu Lys Pro Asp Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His Phe  
 145 150 155 160  
 Lys Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asn Glu Ser Asp  
 165 170 175  
 Pro Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Pro Asn Ala  
 180 185 190  
 Pro Lys Arg Asn Ala Phe Tyr Asp Ala Leu Asn Ser Ile Glu Pro Val  
 195 200 205  
 Ile Gly Gly Gly Ser Val Lys Asn Thr Leu Gly Tyr Asn Ile Lys Asn  
 210 215 220  
 Lys Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu Asn  
 225 230 235 240  
 Ser Gln Gly Tyr Gly Tyr  
 245

<210> 76  
 <211> 247  
 <212> PRT  
 <213> *Helicobacter pylori*

<220>  
 <223> *H. pylori* strain 19C2 FutB fucosyltransferase  
 positions 1-247 (ORF19C2B.pep)

<400> 76  
 Met Phe Gln Pro Leu Leu Asp Ala Tyr Ile Asp Ser Thr Arg Leu Asp  
 1 5 10 15  
 Glu Thr Asp Tyr Lys Pro Pro Leu Asn Ile Ala Leu Ala Asn Trp Trp  
 20 25 30  
 Pro Leu Asp Lys Arg Glu Ser Lys Gly Phe Arg Lys Lys Phe Ile Leu  
 35 40 45  
 His Phe Ile Leu Ser Gln His Tyr Thr Ile Ala Leu His Arg Asn Pro  
 50 55 60  
 Asp Lys Pro Ala Asp Ile Val Phe Gly Asn Pro Leu Gly Ser Ala Arg  
 65 70 75 80  
 Lys Ile Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu  
 85 90 95  
 Asn Glu Val Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp  
 100 105 110  
 Glu Leu Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Asp  
 115 120 125  
 Arg Leu His His Lys Ala Glu Ser Val Asn Asp Thr Thr Ala Pro Tyr  
 130 135 140  
 Lys Ile Lys Ser Asp Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His  
 145 150 155 160



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<220>
<221> MOD_RES
<222> (41)
<223> Xaa = Lys or Glu

<220>
<221> MOD_RES
<222> (42)
<223> Xaa = Lys, Glu or Ser

<220>
<221> MOD_RES
<222> (43)
<223> Xaa = Lys or absent

<220>
<221> MOD_RES
<222> (44)
<223> Xaa = Gly or absent

<220>
<221> MOD_RES
<222> (45)
<223> Xaa = Phe or absent

<220>
<221> MOD_RES
<222> (49)
<223> Xaa = Ser, Asn or Phe

<220>
<221> MOD_RES
<222> (65)
<223> Xaa = Arg or Gln

<220>
<221> MOD_RES
<222> (69)
<223> Xaa = Lys or Glu

<220>
<221> MOD_RES
<222> (102)
<223> Xaa = Val or Ser

<220>
<221> MOD_RES
<222> (131)
<223> Xaa = Ala or Asp

<220>
<221> MOD_RES
<222> (132)
<223> Xaa = Tyr, His or Arg

<220>
<221> MOD_RES
<222> (139)
<223> Xaa = Leu or Ser

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<400> 77															
Met	Phe	Gln	Pro	Leu	Leu	Asp	Ala	Phe	Ile	Glu	Ser	Ala	Xaa	Ile	Glu
1		-		5					10					15	
Lys	Xaa	Xaa	Ser	Lys	Xaa	Xaa	Xaa	Pro	Pro	Leu	Lys	Ile	Ala	Val	Ala
			20					25					30		
Asn	Trp	Trp	Gly	Asp	Glu	Glu	Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Lys	Lys
		35					40					45			
Xaa	Ile	Leu	Tyr	Phe	Ile	Leu	Ser	Gln	His	Tyr	Thr	Ile	Thr	Leu	His
	50					55					60				
Xaa	Asn	Pro	Asx	Xaa	Pro	Ala	Asp	Ile	Val	Phe	Gly	Asn	Pro	Leu	Gly
65					70					75					80
Ser	Ala	Arg	Lys	Ile	Leu	Ser	Tyr	Gln	Asn	Ala	Lys	Arg	Val	Phe	Tyr
				85					90					95	
Thr	Gly	Glu	Asn	Glu	Xaa	Pro	Asn	Phe	Asn	Leu	Phe	Asp	Tyr	Ala	Ile
			100					105					110		
Gly	Phe	Asp	Glu	Leu	Asp	Phe	Arg	Asp	Arg	Tyr	Leu	Arg	Met	Pro	Leu
		115					120					125			
Tyr	Tyr	Xaa	Xaa	Leu	His	His	Lys	Ala	Glu	Xaa	Val	Asn	Asp	Thr	Thr
	130					135					140				
Ser	Pro	Tyr	Lys	Leu	Lys	Xaa	Asp	Ser	Leu	Tyr	Ala	Leu	Lys	Lys	Pro
145				150						155					160
Ser	His	His	Phe	Lys	Glu	Asn	His	Pro	Asn	Leu	Cys	Ala	Val	Val	Asn
				165					170					175	
Asn	Glu	Ser	Asp	Pro	Leu	Lys	Arg	Gly	Phe	Ala	Ser	Phe	Val	Ala	Ser
			180					185					190		
Asn	Pro	Asn	Ala	Pro	Xaa	Arg	Asn	Ala	Phe	Tyr	Asp	Ala	Leu	Asn	Ser
		195					200					205			
Ile	Glu	Pro	Val	Xaa	Gly	Gly	Gly	Ser	Val	Lys	Asn	Thr	Leu	Gly	Tyr
	210					215					220				

Asn Val Lys Asn Lys Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu  
 225 230 235 240

Cys Phe Glu Asn Ser Gln Gly Tyr Gly Tyr  
 245 250

<210> 78  
 <211> 333  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <223> H. pylori strain 915 FutA fucosyltransferase  
 (915A.cod(MWG))

<400> 78  
 atgttccaac ccctattaga tgcctttata gaaagcgctt ccattgaaaa aatggcctct 60  
 aaatctcccc ccctaaaaat cgctgtggcg aattggtggg gagatgaaga aattaaaaaa 120  
 tttaaaaaga gcgttcttta ttttatccta agccagcatt acacaatcac ttacaccga 180  
 aaccctgata aacctgcgga catcgtcttt ggtaaccccc ttggatcagc cagaaaaatc 240  
 ttatcctatc aaaacgcaaa aagggtggtt tacaccggtg aaaatgaagt ccctaacttc 300  
 aacctctttg attacgccat aggcttttga tga 333

<210> 79  
 <211> 1483  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial  
 Sequence:fucosyltransferase consensus sequence

<220>  
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 <222> (77)..(79)  
 <223> n = c or absent

<220>  
 <221> modified\_base  
 <222> (106)..(107)  
 <223> n = c or absent

<220>  
 <221> modified\_base  
 <222> (108)..(110)  
 <223> n = t or absent

<220>  
 <221> modified\_base  
 <222> (119)  
 <223> n = g or absent

<220>  
 <221> modified\_base  
 <222> (152)  
 <223> n = t or absent

<220>  
<221> modified\_base  
<222> (153)  
<223> n = a or absent

<220>  
<221> modified\_base  
<222> (154)  
<223> n = c or absent

<220>  
<221> modified\_base  
<222> (343)  
<223> n = t or absent

<220>  
<221> modified\_base  
<222> (809)..(810)  
<223> n = g or absent

<220>  
<221> modified\_base  
<222> (816)  
<223> n = c or absent

<220>  
<221> modified\_base  
<222> (1063)..(1064)  
<223> n = a or absent

<220>  
<221> modified\_base  
<222> (1065)  
<223> n = c or absent

<220>  
<221> modified\_base  
<222> (1066)  
<223> n = a or absent

<220>  
<221> modified\_base  
<222> (1067)  
<223> n = t or absent

<220>  
<221> modified\_base  
<222> (1068)  
<223> n = c or absent

<220>  
<221> modified\_base  
<222> (1118)  
<223> n = g or absent

<220>  
<221> modified\_base  
<222> (1119)  
<223> n = a or absent

<220>  
 <221> modified\_base  
 <222> (1120)  
 <223> n = t or absent

<400> 79  
 atgttccaac ccctattaga cgcctttata gaaagcgctt ccattgaaaa aatbgcctct 60  
 aaatctcccc ccccmynntt aaaaatcgct gtggcgaatt ggtggnnnnn ggagatgana 120  
 gaaattaaag aattttaaaaa garcdttctt tnnnatTTta tyctaagyca gcattacaca 180  
 atcacycctcc accraaacc yratraacct kcvgaymtcg tctttggyaa yccycttgga 240  
 tcagccagaa aaatcttata ctatcaaaac gcaaaaagrg tgttttacac cggtgaaaaac 300  
 gaakyvccta atttcaacct ctttgattac gccataggct ttngatgaat tggaytttag 360  
 agatcgttat ttragaatgc ctttrtatta tgmyhrwytr cacyataaag ccgagmkygt 420  
 kaatgacacc actkcgctt acaaactcaa abctgacagc ctttatgctt taaaaaaacc 480  
 ctcccacatc tttaaagaaa accaccchaa ttrtgcgca gtagtgaaya atgagagcga 540  
 tcctttgaaa agagggtttg cgagytttgt mgcragcaac cctaacgctc ctadaaggaa 600  
 ygcttttytat gasgctttta attctatwga gccagttayt gggggaggga gcgtgaraaa 660  
 cacttttaggc tataabrtya aaaacaarag cgagttttta agccaatata arttcaatct 720  
 gtgttttgaa aacwcdcaag gctatggcta tgtaactgaa aaaatcattg acgcttaytt 780  
 yagccatacc attcctattt attgggggnn agtccnyagc gtggcrmaag attttaaccc 840  
 taaragtttt gtgaatgtby rtgatttyaa mraytttgat gaagcgattg ayyatrtsmr 900  
 atacytgcac acgcacccaa acgcttattt agacatgcwy tatgaaaacc ctttaaacac 960  
 ymttgatggg aaagcttact tttaccaara tttgagtttt aaaaaaatcc tagatttttt 1020  
 taaaacgaty ttagaaaacg ayacgatyta tcacrawwwc ycnnnnnntt tyatktkbka 1080  
 kyrygatytg matragcckt yartatcyat tgatgrtnnn ttgagggtta attatgatga 1140  
 tttgagggtt aattatgays rkytkwkrsw waaykmtkmk smtttrwkrw wmwytmtsa 1200  
 dvryhybwbd bwwaahdhk mksvywwrdb dkwwywhmw bmhdwbhybw bkktkmrhdh 1260  
 bkwwkvrhwwr dbkkwtmaww awkhbkdkyy kwdrktkmrt kvyrwwrrkw krwgggttaa 1320  
 wwakkawgat ttgagggtta attatgagcg gctcttacia aacgcctcgc ctttattaga 1380  
 actctctcaa aacaccactt ttaaaatcta tcgcaaagct tatcaaaaat ccttaccttt 1440  
 gttgcgtgcg gcgagaaagt tgattaaaaa attggggttg taa 1483

<210> 80  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:"FLAG tag"  
 epitope tag recognized by anti-LAG antibody

<400> 80  
 Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5

<210> 81  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:polyhistidine  
 metal chelate affinity purification tag,  
 hexahistidine affinity tag

<400> 81  
 His His His His His His  
 1 5